

SEQUENCE LISTING

<110> Ema, Hideo
Nakauchi, Hiromitsu
Osawa, Mitsujiro

<120> PROTEIN SUSTAINING UNDIFFERENTIATED STEM CELLS

<130> 790086.405USPC

<140> US 10/507,343
<141> 2002-03-11

<150> PCT/JP02/02265
<151> 2002-03-11

<160> 27

<170> PatentIn Ver. 2.1

<210> 1
<211> 1140
<212> DNA
<213> Mus musculus

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<211> 379
<212> PRT
<213> Mus musculus

<400> 2

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Arg	Ala	Asp	Ala													
Gly	Gln	Pro	Pro													
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Glu	Glu	Ser	Leu	Tyr	Leu	Trp	Ile	Asp	Ala	His	Gln	Ala	Arg	Val	Leu	
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His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln	
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Cys	Asp	Lys	Ala	Asn	Cys	Ser	Thr	Thr	Cys	Phe	Asn	Gly	Gly	Thr	Cys	
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Phe	Tyr	Pro	Gly	Lys	Cys	Ile	Cys	Pro	Pro	Gly	Leu	Glu	Gly	Gln		
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Cys	Glu	Leu	Ser	Lys	Cys	Pro	Gln	Pro	Cys	Arg	Asn	Gly	Gly	Lys	Cys	
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290

295

300

Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320

His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335

Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350

Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 3

<211> 1140

<212> DNA

<213> Homo sapiens

<400> 3

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<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
 145 150 155 160

Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175

Cys Leu Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190

Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
 195 200 205

Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220

Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255

Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270

Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285

Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
 290 295 300

Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320

His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
 325 330 335

Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
 340 345 350

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
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Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 5

<211> 1098

<212> DNA

<213> Rattus norvegicus

<400> 5

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<211> 365

<212> PRT

<213> Rattus norvegicus

<400> 6

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ser Gly Gln
 85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Arg Leu Gly Thr Val Pro
 115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160

Gly Asn Pro Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175

Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190

Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 195 200 205

Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220

Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240

Cys Asp Lys Ala Asn Cys Ser Ala Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255

Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270

Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285

Ile Gly Lys Ser Lys Ser Val Cys Glu Pro Gly Cys Gly Ala His Gly
 290 295 300

Thr Cys His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly
 305 310 315 320

Arg His Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg
 325 330 335

Pro Ala Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala
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Glu Gly Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
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<210> 7
 <211> 1125
 <212> DNA
 <213> Xenopus sp.

<400> 7

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<210> 8
 <211> 374
 <212> PRT
 <213> Xenopus sp.

<400> 8

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 35 40 45

Asp Ile Leu Ile Val Ala Glu Gly Lys Met Ala Pro Phe Thr His Asp

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Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile Pro Val Asn Ile His			
65	70	75	80
Ala Met Asn Phe Thr Trp Gln Ala Thr Gly Gln Ala Glu Tyr Phe Tyr			
85	90	95	
Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro			
100	105	110	
Thr Val Asn Met Pro Leu Leu Gly Thr Val Pro His Lys Ala Thr Val			
115	120	125	
Ile Gln Val Gly Phe Pro Cys Leu Gly Asn Gln Asp Gly Val Ala Ala			
130	135	140	
Phe Glu Val Asn Val Ile Val Met Asn Ser Glu Gly Asn Val Ile Leu			
145	150	155	160
Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala Lys			
165	170	175	
Cys Thr Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Asp Arg His Val			
180	185	190	
Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His Cys Glu Lys Ala Leu			
195	200	205	
Cys Met Pro Arg Cys Met Asn Gly Gly Leu Cys Val Thr Pro Gly Leu			
210	215	220	
Cys Ile Cys Pro Pro Gly Tyr Tyr Gly Ile Asn Cys Asp Lys Val Asn			
225	230	235	240
Cys Thr Thr His Cys Leu Asn Gly Gly Thr Cys Phe Tyr Pro Gly Lys			
245	250	255	
Cys Ile Cys Pro Ser Gly Tyr Glu Gly Glu Gln Cys Glu Thr Ser Lys			
260	265	270	
Cys Gln Gln Pro Cys Arg Asn Gly Gly Lys Cys Ser Gly Lys Asn Lys			
275	280	285	
Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu Cys Ser Lys Pro Val			
290	295	300	
Cys Glu Pro Ser Cys Gly Ala His Gly Thr Cys Ile Glu Pro Asn Lys			
305	310	315	320
Cys Gln Cys Lys Glu Gly Trp Asn Gly Arg Tyr Cys Asn Lys Lys Tyr			
325	330	335	
Gly Ser Asn Leu Met Asn Ala Leu Arg Pro Thr Gly Ser Arg Asn Arg			

340

345

350

Gln His Thr Pro Ser Pro Lys Arg Thr Glu Asp Arg Gln Ala Leu Pro
 355 360 365

Glu Ser Asn Tyr Ile Trp
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<210> 9
<211> 1137
<212> DNA
<213> Danio rerio

<400> 9

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<210> 10
<211> 378
<212> PRT
<213> Danio rerio

<400> 10

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Thr Met Tyr Met Trp Ile Asp Ala Asn Gln Ala Arg Ile Leu Ile Gly
 35 40 45

Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala Pro Phe
 50 55 60

Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile Pro Val
 65 70 75 80

Asn Ile His His Val Asn Phe Thr Trp Gln Ala Thr Asp Gln Ala Glu
 85 90 95

Tyr Phe Tyr Glu Phe Gln Thr Leu Arg Ser Leu Asp Lys Asp Ile Met
 100 105 110

Asp Asp Pro Thr Val Asn Val Pro Leu Leu Gly Ser Val Pro His Lys
 115 120 125

Ala Ser Val Val Gln Val Gly Phe Pro Cys Arg Gly Asp Gln Asp Gly
 130 135 140

Val Ala Ala Phe Glu Val Thr Ile Leu Val Met Asp Ala Gly Gly Asn
 145 150 155 160

Ile Ile Leu Arg Thr Pro His Asn Ala Ile Phe Phe Lys Thr Cys Gln
 165 170 175

Arg Ala Lys Cys Pro Gly Gly Cys Arg Asn Gly Gly Tyr Cys Asn Glu
 180 185 190

Arg Gln Val Cys Glu Cys Gln Asp Gly Phe Tyr Gly Val His Cys Glu
 195 200 205

Lys Ala Leu Cys Ser Pro Arg Cys Leu Asn Gly Gly Leu Cys Met Ser
 210 215 220

Pro Gly Val Cys Ile Cys Pro Pro Gly Tyr Phe Gly Ser Ser Cys Glu
 225 230 235 240

Arg Ala Asn Cys Ser Thr Thr Cys Leu Asn Gly Gly Thr Cys Phe His
 245 250 255

Pro Gly Lys Cys Ile Cys Ala Val Ser Phe Glu Gly Val Arg Cys Glu
 260 265 270

Leu Ser Lys Cys Arg Gln Pro Cys Arg Asn Gly Gly Lys Cys Thr Gly
 275 280 285

Arg Asn Lys Cys Lys Cys Ser Lys Gly Tyr His Gly Asp Leu Cys Ser
 290 295 300

Lys Ala Val Cys Glu Pro Ser Cys Gly Ala His Gly Thr Cys Val Glu
 305 310 315 320

Pro Asn Arg Cys Gln Cys Arg Glu Gly Trp His Gly Arg His Cys Asn
 325 330 335

Lys Arg Phe Arg Gly Gly Val Ser Asn Ser Gln Arg Val Ser Pro Ser
 340 345 350

Lys His Lys Ser Pro Ser Val Ala Ala Ala Lys Glu Ala Pro Glu Thr
 355 360 365

Ser Gln Pro Ser Glu Thr Asn Tyr Val Val
 370 375

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial Sequence

<400> 11 26
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<210> 12
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial Sequence

<400> 12 26
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<210> 13
<211> 4817
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:pCAGGS 6xHis construct

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 cactcgtgca cccaaactgtat cttcagcatc ttttactttc accagcggtt ctgggtgagc 4620
 aaaaacagga aggcaaaatg cgcacaaaaaa ggaaataagg gcacacggaa aatgttgaat 4680
 actcataactc ttccttttc aatattattt aagcattttt cagggttatt gtctcatgag 4740
 cgatatacata tttgaatgtt ttttagaaaaaa taaacaaata ggggttccgc gcacattcc 4800
 ccgaaaatgtt ccacctg 4817

<210> 14
 <211> 1140
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Artificial Sequence

<400> 14
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 ctgctcctgc tgcgagcgga tgcaggcgag ccacctgagg agagcttgc cctgtggatc 120
 gacgcccattc aggcttagt gctcatagga tttgaagaag accttctgtat tgtctcgag 180
 gggaaaatgg ccccctttac acatgatttc agggaaagccc aacaaagaat gccagccatt 240
 cctgtcaata tccactccat gaattttacc tggcaagctg cggggcaggc agaatacttc 300
 tacgagttcc tgcgtctgcg ctccctggat aaaggcatca tggcagatcc aactgtcaat 360
 gtcccttgc tggaaacagt gcctcacaag gcatcagttg ttcaagttgg tttccctgt 420
 ctcggcaaac aagacggggt agcagcatt gaagtgaatg tgattgtcat gaattctgaa 480
 gccaacacca tccttaggac ccctcagaat gccatcttct taaaacatg tcaacaagct 540
 gagtgccccg gagggtgtcg aaatggaggc tttttaacg aaaggcggtt ctgcgagtgt 600
 cccgatgggt tctacgggcc tcactgttagt aaagccctgt gcatccccg atgtatgaac 660
 ggtggctgt gtgtcactcc tggcttctgc atctgcccccc ctggattctt cgggtcaac 720
 tgcgtacaaag caaactgttc aaccacctgc ttaatggag ggacctgtt ttacccggga 780
 aaatgtatcc gcccctctgg actcgaggga gaggcgtgtg aactcagcaa atgcccccaa 840
 ccctgcccggaa atggaggtaa atgcatttgtt aaaagcaagt gtaagtccc gaaaggttac 900
 caaggagacc tgcgtctaa gcccgtctgc gaggctggct gtgggtccca cggacaccc 960
 cacgaaccca acaagtgcctt gttcgagag ggctggcaccg gcagacactg caataagagg 1020
 tatggagccca gcctcatgca tggcccgagg ccagcaggcg ccggcgttgc ggcacaccc 1080
 ctttcactta aaaaggctga ggtatagaagg gatccacccat aatccaaatcatctggta 1140

<210> 15
 <211> 379
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 15
Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
1 5 10 15

Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
35 40 45

Ile Gly Phe Glu Glu Asp Leu Leu Ile Val Ser Glu Gly Lys Met Ala
50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
145 150 155 160

Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
165 170 175

Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
180 185 190

Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
195 200 205

Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
210 215 220

Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
225 230 235 240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
245 250 255

Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
260 265 270

Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285

Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300

Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320

His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335

Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350

Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 16

<211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 16

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 ctgctcctgc tgcgagcgga tgcaggcgag ccacctgagg agagcttgta cctgtggatc 120
 gacgcccattc aggcttaggt gctcatagtaga tttgaagaag acattctgtat tgtctcgag 180
 gggaaaaatgg ccccctttac acatgatttc agggaaagccc aacaaagaat gccagccatt 240
 cctgtcaata tccactccat gaattttacc tggcaagctg cggggcagggc agaataactc 300
 tacgagttcc tgtctctgcttccattgtat aaaggcatca tggcagatcc aactgtcaat 360
 gtccctttgc tgggaacagt gcctcacaag gcatcagttg ttcaagttgg tttccctgt 420
 ctcggcaaac aagacgggtt agcagcattt gaagtgaatg tgattgtcat gaattctgaa 480
 gccaacaccca tccttaggac ccctcagaat gccatcttct taaaacatg tcaacaagct 540
 gagtgtccccg gagggtgtcg aaatggaggc tttttaacg aaaggcggtt ctgcgagtgt 600
 cccggatgggt tctacgggcc tcactgttagt aaagccctgt gcataccccc atgtatgaac 660
 ggtggctgtgt gtgtcaactcc tggcttctgc atctgccccctt ctggattcta cggtgtcaac 720
 tgtgacaaag caaactgctc aaccacctgc tttaatggag ggacctgctt ttacccggga 780
 aaatgtattt gccctcctgg actcgaggaa gagcagtgtg aactcagcaa atgcccccaa 840
 ccctggcgaa atggaggtaa atgcatttgtt aaaagcaagt gtaagtgcggc gaaagggtac 900
 caaggagacc tgtgctctaa gcccgtctgc gagcctggct gtgggtccca cggaacctgc 960
 cacgaaccca acaagtgcctt gtgtcgagag ggctggcacg gcagacactg caataagagg 1020
 tatggagcca gcctcatgca tgccccgagg ccagcaggcg ccgggctgga ggcacacacg 1080
 ccttcactta aaaaggctga ggatagaagg gatccacactg aatccaatta catctggta 1140

<210> 17
<211> 379
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial Sequence

<400> 17
Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
1 5 10 15

Ile Leu Pro Cys Leu Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
50 55 60

Pro	Phe	Thr	His	Asp	Phe	Arg	Lys	Ala	Gln	Gln	Arg	Met	Pro	Ala	Ile
65					70					75					80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Ile Asp Lys Gly
100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln .
130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
145 150 155 160

Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
165 170 175

Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190

Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
195 200 205

Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
210 215 220

Val	Thr	Pro	Gly	Phe	Cys	Ile	Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Val	Asn
225				230						235					240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255

Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270

Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285

Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300

Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320

His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335

Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350

Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 18

<211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 18

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 ctgctcctgc tgcgagcgga tgcaggcgag ccacctgagg agagcttgta cctgtggatc 120
 gacgccccatc aggcttaggt gctcatagga tttgaagaag acattctgtat tgtctcgag 180
 ggaaaaatgg ccccctttac acatgatttc aggaàagccc aacaaagaat gccagccatt 240
 cctgtcaata tccactccat gaattttacc tggcaagctg cggggcagggc agaatacttc 300
 tacgagttcc tgtctctgcg ctccctggat aaaggcatca tggcagatcc aactgtcaat 360
 gtccctttgc tggAACAGT gcctcacaag gcatcagtgc ttcaagttgg tttccgtgt 420
 ctcggcaaac aagacgggggt agcagcattt gaagtgaatg tgattgtcat gaattctgaa 480
 ggcAACACCA tccttaggac ccctcagaat gccatcttct ttaaaaacatg tcaacaagct 540
 gagtgcccg gagggtgtcg aaatggaggc tttttaacg aaaggcggtt ctgcgagtgt 600
 ccggatgggt tctacgggcc tcactgttag aaagccctgt gcataccccg atgtatgaac 660
 ggtggctgtgtgtcaactcc tggcttctgc atctgccccctt ctggattcta cggtgtcaac 720
 tttgacaaag taaactgctc aaccacctgc tttaatggag ggacctgtttt ttacccggaa 780
 aaatgtattt gcccctcctgg actcgaggga gagcagtgtg aactcagcaa atgcccccaa 840
 ccctggcgaa atggaggtaa atgcattggt aaaagcaagt gtaagtgcc gaaaggttac 900

caaggagacc tgtgctctaa gcccgtctgc gagcctggct gtggtgccca cggaacctgc 960
 cacgaaccca acaagtgcc a gtgtcgagag ggctggcacg gcagacactg caataagagg 1020
 tatggagcca gcctcatgca tgccccgagg ccagcaggcg ccgggctgga ggcacacacg 1080
 ctttcactta aaaaggctga ggatagaagg gatccacactg aatccaattt catctggtga 1140

<210> 19
 <211> 379
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Artificial Sequence

<400> 19
 Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 1 5 10 15

Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160

Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175

Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190

Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 195 200 205

Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220

Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240

Cys Asp Lys Val Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255

Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270

Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285

Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300

Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320

His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335

Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350

Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 20
<211> 1140
<212> _DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial Sequence

<400> 20
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ctgctcctgc tgcgagcgga tgcaggcag ccacctgagg agagcttcta cctgtggatc 120
gacgcccatac aggcttagt gctcatagga tttgaagaag acattctgtat tgtctcgag 180
ggaaaaatgg ccccctttac acatgatttc aggaaagccc aacaaagaat gccagccatt 240
cctgtcaata tccactccat gaattttacc tggcaagctg cggggcagggc agaatacttc 300
tacgagttcc tgtctctgcg ctccctggat aaaggcatca tggcagatcc aactgtcaat 360
gtccctttgc tggaaacagt gcctcacaag gcatcagttg ttcaagttgg tttcccggt 420
ctcggcaaac aagacggggt agcagcatt gaagtgaatg tgattgtcat gaattctgaa 480
ggcaacacca tccttaggac ccctcagaat gccatcttct ttaaaaacatg tcaacaagct 540

gagtgtcccg gagggtgtcg aaatggaggc tttttaacg aaaggcggtt ctgcgagtgt 600
 ccggatgggt tctacgggcc tcactgttag aaagccctgt gcatacccg atgtatgaac 660
 ggtggctgt gtgtcaactcc tggcttctgc atctgccccctt cggattcta cggtgtcaac 720
 tgtgacaaag caaactgctc aaccacctgc ttatggag ggacctgctt ttacccggaa 780
 aaatgtattt gccctcctgg actcgaggaa gatcagtgtg aactcagcaa atgcccccaa 840
 ccctgccgaa atggaggtaa atgcattgtt aaaagcaagt gtaagtgcgc gaaaggttac 900
 caaggagacc tgtgctctaa gcccgtctgc gagcctggct gtggtgccca cggaacctgc 960
 cacgaaccca acaagtgcgc gtgtcgagag ggctggcacg gcagacactg caataagagg 1020
 tatggagcca gcctcatgca tgccccgagg ccagcaggcg ccgggctgga gcgacacacg 1080
 ccttcactta aaaaggctga ggatagaagg gatccacctg aatccaatta catctggta 1140

<210> 21

<211> 379

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 21

Met	Ala	Arg	Arg	Arg	Ala	Phe	Pro	Ala	Phe	Ala	Leu	Arg	Leu	Trp	Ser
1		5					10							15	

Ile	Leu	Pro	Cys	Leu	Leu	Leu	Leu	Arg	Ala	Asp	Ala	Gly	Gln	Pro	Pro
				20				25					30		

Glu	Glu	Ser	Leu	Tyr	Leu	Trp	Ile	Asp	Ala	His	Gln	Ala	Arg	Val	Leu
						35		40					45		

Ile	Gly	Phe	Glu	Glu	Asp	Ile	Leu	Ile	Val	Ser	Glu	Gly	Lys	Met	Ala
						50		55					60		

Pro	Phe	Thr	His	Asp	Phe	Arg	Lys	Ala	Gln	Gln	Arg	Met	Pro	Ala	Ile
						65		70					75		80

Pro	Val	Asn	Ile	His	Ser	Met	Asn	Phe	Thr	Trp	Gln	Ala	Ala	Gly	Gln
						85			90					95	

Ala	Glu	Tyr	Phe	Tyr	Glu	Phe	Leu	Ser	Leu	Arg	Ser	Leu	Asp	Lys	Gly
							100		105				110		

Ile	Met	Ala	Asp	Pro	Thr	Val	Asn	Val	Pro	Leu	Leu	Gly	Thr	Val	Pro
						115		120					125		

His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln
						130		135				140			

Asp	Gly	Val	Ala	Ala	Phe	Glu	Val	Asn	Val	Ile	Val	Met	Asn	Ser	Glu
						145		150				155			160

Gly	Asn	Thr	Ile	Leu	Arg	Thr	Pro	Gln	Asn	Ala	Ile	Phe	Phe	Lys	Thr
						165			170				175		

Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190

Asn Glu Arg Arg Val Cys Glu Cys Pro Asp Gly Phe Tyr Gly Pro His
 195 200 205

Cys Glu Lys Ala Leu Cys Ile Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220

Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240

Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255

Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Asp Gln
 260 265 270

Cys Glu Leu Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285

Ile Gly Lys Ser Lys Cys Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu
 290 295 300

Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320

His Glu Pro Asn Lys Cys Gln Cys Arg Glu Gly Trp His Gly Arg His
 325 330 335

Cys Asn Lys Arg Tyr Gly Ala Ser Leu Met His Ala Pro Arg Pro Ala
 340 345 350

Gly Ala Gly Leu Glu Arg His Thr Pro Ser Leu Lys Lys Ala Glu Asp
 355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
 370 375

<210> 22

<211> 558

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificial Sequence

<400> 22

atggctcgga gaagagcatt ccctgctttc gcgcgtccggc tctggagcat cctaccttgc 60
 ctgctcctgc tgcgagcgaa tgcaggcgac ccacctgagg agagcttgta cctgtggatc 120
 gacgccccatc aggctagagt gctcatagga tttgaagaag acattctgat tgtctcgag 180

ggaaaaatgg ccccccattac acatgatttc aggaaagccc aacaaagaat gccagccatt 240
 cctgtcaata tccactccat gaattttacc tggcaagctg cggggcaggc agaatacttc 300
 tacgagttcc tgtctctgcg ctccctggat aaaggcatca tggcagatcc aactgtcaat 360
 gtcccttgc tgggaacagt gcctcacaag gcatcagttg ttcaagttgg tttccgtgt 420
 ctcggcaaac aagacggggt agcagcatt gaagtgaatg tgattgtcat gaattctgaa 480
 gccaacacca tccttaggac ccctcagaat gccatcttct ttaaaaacaca gctagcccat 540
 catcatcatc atcattga 558

<210> 23
 <211> 185
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Artificial Sequence

<400> 23
 Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
 1 5 10 15

Ile Leu Pro Cys Leu Leu Leu Arg Ala Asp Ala Gly Gln Pro Pro
 20 25 30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80

Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95

Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110

Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125

His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140

Asp Gly Val Ala Ala Phe Glu Val Asn Val Ile Val Met Asn Ser Glu
 145 150 155 160

Gly Asn Thr Ile Leu Arg Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175

Gln Leu Ala His His His His His
 180 185

<210> 24
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial Sequence

<400> 24
atggctcgga gaagagcctt ccctgctttc gcgcgtccggc tctggagcat cctaccttgc 60
ctgctcctgc tgctcgactg tcaacaagct gagtgtcccg gagggtgtcg aaatggaggc 120
ttttgttaacg aaaggcggt ctgcgagtg ccggatgggt tctacgggcc tcactgttag 180
aaagccctgt gcataccccg atgtatgaac ggtggtctgt gtgtcactcc tggcttctgc 240
atctgccccctt ctggattcta cggtgtcaac tgtgacaaag caaactgttc aaccacctgc 300
tttaatggag ggacctgctt ttacccggga aaatgtattt gcccctctgg actcgaggga 360
gagcagtgtg aactcagcaa atgcccccaa ccctgcccga atggaggtaa atgcattgg 420
aaaagcaagt gtaagtgccc gaaaggttac caaggagacc tgtgctctaa gcccgctctgc 480
gagcctggct gtgggccca cggAACCTGC cacgaaccca acaagtgcac gtgtcgagag 540
ggctggcacg gcagacactg caataagagg tatggagcca gcctcatgca tgccccgagg 600
ccagcaggcg ccgggtctggc ggcacacacg ctttactta aaaaggctga ggatagaagg 660
gatccacctg aatccaatta catctggcag ctggccatc atcatcatca tcattga 717

<210> 25
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificial Sequence

<400> 25
Met Ala Arg Arg Arg Ala Phe Pro Ala Phe Ala Leu Arg Leu Trp Ser
1 5 10 15

Ile Leu Pro Cys Leu Leu Leu Leu Asp Cys Gln Gln Ala Glu Cys
20 25 30

Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg Arg Val Cys
35 40 45

Glu Cys Pro Asp Gly Phe Tyr Gly Pro His Cys Glu Lys Ala Leu Cys
50 55 60

Ile Pro Arg Cys Met Asn Gly Gly Leu Cys Val Thr Pro Gly Phe Cys
65 70 75 80

Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn Cys Asp Lys Ala Asn Cys
85 90 95

Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys Phe Tyr Pro Gly Lys Cys
 100 105 110

Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln Cys Glu Leu Ser Lys Cys
 115 120 125

Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys Ile Gly Lys Ser Lys Cys
 130 135 140

Lys Cys Pro Lys Gly Tyr Gln Gly Asp Leu Cys Ser Lys Pro Val Cys
 145 150 155 160

Glu Pro Gly Cys Gly Ala His Gly Thr Cys His Glu Pro Asn Lys Cys
 165 170 175

Gln Cys Arg Glu Gly Trp His Gly Arg His Cys Asn Lys Arg Tyr Gly
 180 185 190

Ala Ser Leu Met His Ala Pro Arg Pro Ala Gly Ala Gly Leu Glu Arg
 195 200 205

His Thr Pro Ser Leu Lys Lys Ala Glu Asp Arg Arg Asp Pro Pro Glu
 210 215 220

Ser Asn Tyr Ile Trp Gln Leu Ala His His His His His His
 225 230 235

<210> 26
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> WIF-1 repeat

<221> VARIANT
 <222> 2, 3, 4, 6, 7, 8, 9, 10, 12, 13, 14, 15, 16, 18, 20, 21,
 22, 23, 24, 25, 26, 27, 29, 30, 31, 32
 <223> Xaa = Any Amino Acid

<400> 26
 Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
 1 5 10 15
 Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
 20 25 30

<210> 27
 <211> 36
 <212> PRT
 <213> UNKNOWN

<220>

<223> Specific domain in the epidermal growth factor which comprises the EGF like repeat

<221> VARIANT

$\langle 2222 \rangle = 2, 3, 4, 5, 6, 7, 8, 10, 11, 12, 13, 15, 16, 17, 18, 19,$
 $20, 21, 22, 23, 24, 26, 28, 29, 30, 31, 32, 33, 34, 35$

<223> Xaa = Any Amino Acid

<400> 27